

Patent Application US/07/978,891

SEQUENCE LISTING

see pp. 1, 4 → 16

1
2
3
4 (1) GENERAL INFORMATION
5
6 (i) APPLICANT: Darrell Anderson, Nabil Hanna, John Leonard, Roland Newman and Mitchell R
7
8 (ii) TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC ANTIBODY TO HUMAN B LYMPHOCY
9
10 (iii) NUMBER OF SEQUENCES: 8
11
12 (iv) CORRESPONDING ADDRESS:
13
14 (A) ADDRESSEE: IDEC Pharmaceuticals Corporation
15 (B) STREET: 11099 N. Torrey Pines Road, #160
16 (C) CITY: La Jolla
17 (D) STATE: California
18 (E) COUNTRY: USA
19 (F) ZIP: 92037
20
21 (v) COMPUTER READABLE FORM:
22
23 (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
24 (B) COMPUTER: Macintosh
25 (C) OPERATING SYSTEM: MS.DOS
26 (D) SOFTWARE: Microsoft Word 5.0
27 *← insert ending parenthesis*
28 (vi) CURRENT APPLICATION DATA:
29
30 (A) APPLICATION NUMBER:
31 (B) FILING DATE:
32 (C) CLASSIFICATION:
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35
36 (A) NAME: Burgoon, Richard P. Jr.
37 (B) REGISTRATION NUMBER: 34,787
38 (C) REFERENCE/DOCKET NUMBER:
39
40 (ix) TELECOMMUNICATION INFORMATION:
41
42 (A) TELEPHONE: (619) 458-0600
43 (B) TELEFAX: (619) 546-9274
44
45
46 (2) INFORMATION FOR SEQ. ID NO.: 1:
47
48 (i) SEQUENCE CHARACTERISTICS:
49
50 (A) LENGTH: 8540 bases
51 (B) TYPE: nucleic acid
52 (C) STRANDEDNESS: single

*Delete periods -
Edit this error
throughout the
remaining seq.
listings*

LINE ORIGINAL TEXT

CORRECTED TEXT

4 (1)GENERAL INFORMATION
12 (iv)CORRESPONDING ADDRESS:
46 (2)INFORMATION FOR SEQ. ID. NO.: 1:
61 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.:
351 (3)INFORMATION FOR SEQ. ID. NO.: 2:
366 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.:
677 (4)INFORMATION FOR SEQ. ID. NO.: 3:
692 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.:
698 (5)INFORMATION FOR SEQ. ID. NO.: 4:
713 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.:
719 (6)INFORMATION FOR SEQ. ID. NO.: 5:
734 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.:
754 (7)INFORMATION FOR SEQ. ID. NO.: 6:
769 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.:
777 (8)INFORMATION FOR SEQ. ID. NO.: 7:
792 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.:
797 (9)INFORMATION FOR SEQ. ID. NO.: 8:
812 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.:

(1) GENERAL INFORMATION:
(iv) CORRESPONDENCE ADDRESS:
(2) INFORMATION FOR SEQ ID NO: 1:
(ix) SEQUENCE DESCRIPTION: SEQ ID. NO:
(2) INFORMATION FOR SEQ ID NO: 2:
(ix) SEQUENCE DESCRIPTION: SEQ ID. NO:
(2) INFORMATION FOR SEQ ID NO: 3:
(ix) SEQUENCE DESCRIPTION: SEQ ID. NO:
(2) INFORMATION FOR SEQ ID NO: 4:
(ix) SEQUENCE DESCRIPTION: SEQ ID. NO:
(2) INFORMATION FOR SEQ ID NO: 5:
(ix) SEQUENCE DESCRIPTION: SEQ ID. NO:
(2) INFORMATION FOR SEQ ID NO: 6:
(ix) SEQUENCE DESCRIPTION: SEQ ID. NO:
(2) INFORMATION FOR SEQ ID NO: 7:
(ix) SEQUENCE DESCRIPTION: SEQ ID. NO:
(2) INFORMATION FOR SEQ ID NO: 8:
(ix) SEQUENCE DESCRIPTION: SEQ ID. NO:

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/978,891

DATE: 12/16/92
TIME: 09:46:26
S4267

MANDATORY IDENTIFIER THAT WAS NOT FOUND

CURRENT APPLICATION DATA
APPLICATION NUMBER
FILING DATE
CLASSIFICATION
PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/978,891

DATE: 12/16/92
TIME: 09:46:26
S4267

LINE ERROR

ORIGINAL TEXT

28 Response Exceeds Line Limitations
30 Unknown or Misplaced Identifier
31 Unknown or Misplaced Identifier
32 Unknown or Misplaced Identifier
695 Wrong Nucleic Acid Designator
692 Entered and Calc. Seq. Length differ
716 Wrong Nucleic Acid Designator
734 Entered and Calc. Seq. Length differ
772 Wrong Nucleic Acid Designator
794 Wrong Nucleic Acid Designator
792 Entered and Calc. Seq. Length differ
812 Entered and Calc. Seq. Length differ

(v) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

TC 3' 2

(ix) SEQUENCE DESCRIPTION: SEQ. ID. NO.:

5' TGC AGC ATC CGT ACG TTT GAT TTC CAG C

(ix) SEQUENCE DESCRIPTION: SEQ. ID. NO.:

5' GCG GCT CCC ACG CGT GTC CTG TCC CAG 3

5' GG(G/C) TGT TGT GCT AGC TG(A/C) (A/G)

(ix) SEQUENCE DESCRIPTION: SEQ. ID. NO.:

(ix) SEQUENCE DESCRIPTION: SEQ. ID. NO.:

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53 (D) TOPOLOGY: circular
54
55 (ii) MOLECULE TYPE: DNA (genomic)
56
57 (iii) HYPOTHETICAL: yes
58
59 (iv) ANTI-SENSE: no
60
61 (ix) SEQUENCE DESCRIPTION: SEQ. ID. NO.: 1:
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63 GACGTCGCGG CCGCTCTAGG CCTCCAAAA AGCCTCCTCA CTA CTCTCTGG AATAGCTCAG 60
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65 AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
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67 GGAGAATGGG CGGAAGTGGG CGGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT 180
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81 TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600
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83 AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTG TGCCAGTAC 660
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103 CTCCAATCGG GTA ACTCCCA GGAGAGTGTC ACAGAGCAGG ACAGCAAGGA CAGCACCTAC 1260
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351 (3) INFORMATION FOR SEQ. ID. NO.: 2:

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353 (i) SEQUENCE CHARACTERISTICS:

354
355 (A) LENGTH: 9209 bases

356 (B) TYPE: nucleic acid

357 (C) STRANDEDNESS: single

358 (D) TOPOLOGY: circular

359
360 (ii) MOLECULE TYPE: DNA (genomic)

361
362 (iii) HYPOTHETICAL: yes

363
364 (iv) ANTI-SENSE: no

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366 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.: 2:
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371 AGGCCGAGGC GGCCTCGGCC TCTGCATAAA TAAAAAAAT TAGTCAGCCA TGCATGGGGC 120
372
373 GGAGAATGGG CGGAAC TGGG CGGAGTTAGG GCGGGGATGG GCGGAGTTAG GGGCGGGACT 180
374
375 ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG 240
376
377 GACTTTCCAC ACCTGGTTGC TGA CTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
378
379 GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAT TAATCCCCCT 360
380
381 AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC 420
382
383 GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCAT TG 480
384
385 ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA 540
386
387 TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA TCATATGCCA 600
388
389 AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATT A TGCCCAGTAC 660
390
391 ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC 720
392
393 ATGGTGATGC GGT TTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA 780
394
395 TTTCCAAGTC TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG 840
396
397 GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG TAGGCGTGTA 900
398
399 CGGTGGGAGG TCTATATAAG CAGAGCTGGG TACGTGAACC GTCAGATCGC CTGGAGACGC 960
400
401 CATCACAGAT CTCTCACTAT GGATTTTCAG GTGCAGATTA TCAGCTTCCT GCTAATCAGT 1020
402
403 GCTTCAGTCA TAATGTCCAG AGGACAAATT GTTCTCTCCC AGTCTCCAGC AATCCTGTCT 1080
404
405 GCATCTCCAG GGGAGAAGGT CACAATGACT TGCAGGGCCA GCTCAAGTGT AAGTTACATC 1140
406
407 CACTGGTTCC AGCAGAAGCC AGGATCCTCC CCCAAACCCT GGATTTATGC CACATCCAAC 1200
408
409 CTGGCTTCTG GAGTCCCTGT TCGCTTCAGT GGCAGTGGGT CTGGGACTTC TTA CTTCTCTC 1260
410
411 ACAATCAGCA GAGTGGAGGC TGAAGATGCT GCCACTTATT ACTGCCAGCA GTGGACTAGT 1320
412
413 AACCACCCA CGTTCGGAGG GGGGACCAAG CTGGAAATCA AACGTACGGT GGCTGCACCA 1380
414
415 TCTGTCTTCA TCTTCCCGCC ATCTGATGAG CAGTTGAAAT CTGGAAC TGC CTCTGTTGTG 1440
416

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417	TGCCTGCTGA	ATAACTTCTA	TCCCAGAGAG	GCCAAAGTAC	AGTGGAAGGT	GGATAACGCC	1500
418							
419	CTCCAATCGG	GTAAC TCCA	GGAGAGTGTC	ACAGAGCAGG	ACAGCAAGGA	CAGCACCTAC	1560
420							
421	AGCCTCAGCA	GCACCCTGAC	GCTGAGCAAA	GCAGACTACG	AGAAACACAA	AGTCTACGCC	1620
422							
423	TGCGAAGTCA	CCCATCAGGG	CCTGAGCTCG	CCCGTCACAA	AGAGCTTCAA	CAGGGGAGAG	1680
424							
425	TGTTGAATTC	AGATCCGTTA	ACGGTTACCA	ACTACCTAGA	CTGGATTTCGT	GACAACATGC	1740
426							
427	GGCCGTGATA	TCTACGTATG	ATCAGCCTCG	ACTGTGCCTT	CTAGTTGCCA	GCCATCTGTT	1800
428							
429	GTTTGCCCT	CCCCCGTGCC	TTCCTTGACC	CTGGAAGGTG	CCACTCCCAC	TGTCCTTTCC	1860
430							
431	TAATAAAATG	AGGAAATTGC	ATCGCATTGT	CTGAGTAGGT	GTCATTCTAT	TCTGGGGGGT	1920
432							
433	GGGGTGGGGC	AGGACAGCAA	GGGGGAGGAT	TGGGAAGACA	ATAGCAGGCA	TGCTGGGGAT	1980
434							
435	GCGGTGGGCT	CTATGGAACC	AGCTGGGGCT	CGACAGCTAT	GCCAAGTACG	CCCCCTATTG	2040
436							
437	ACGTCAATGA	CGGTAAATGG	CCCGCCTGGC	ATTATGCCCA	GTACATGACC	TTATGGGACT	2100
438							
439	TTCCTACTTG	GCAGTACATC	TACGTATTAG	TCATCGCTAT	TACCATGGTG	ATGCGGTTTT	2160
440							
441	GGCAGTACAT	CAATGGGCGT	GGATAGCGGT	TTGACTCACG	GGGATTTCCA	AGTCTCCACC	2220
442							
443	CCATTGACGT	CAATGGGAGT	TTGTTTTGGC	ACCAAAATCA	ACGGGACTTT	CCAAAATGTC	2280
444							
445	GTAACAACCTC	CGCCCCATTG	ACGCAAATGG	GCGGTAGGCG	TGTACGGTGG	GAGGTCTATA	2340
446							
447	TAAGCAGAGC	TGGGTACGTC	CTCACATTCA	GTGATCAGCA	CTGAACACAG	ACCCGTCGAC	2400
448							
449	ATGGGTTGGA	GCCTCATCTT	GCTCTTCCTT	GTCGCTGTTG	CTACGCGTGT	CCTGTCCCAG	2460
450							
451	GTACAACCTGC	AGCAGCCTGG	GGCTGAGCTG	GTGAAGCCTG	GGGCCTCAGT	GAAGATGTCC	2520
452							
453	TGCAAGGCTT	CTGGCTACAC	ATTTACCAGT	TACAATATGC	ACTGGGTAAA	ACAGACACCT	2580
454							
455	GGTCGGGGCC	TGGAATGGAT	TGGAGCTATT	TATCCCGGAA	ATGGTGATAC	TTCCTACAAT	2640
456							
457	CAGAAGTTCA	AAGGCAAGGC	CACATTGACT	GCAGACAAAT	CCTCCAGCAC	AGCCTACATG	2700
458							
459	CAGCTCAGCA	GCCTGACATC	TGAGGACTCT	GCGGTCTATT	ACTGTGCAAG	ATCGACTTAC	2760
460							
461	TACGGCGGTG	ACTGGTACTT	CAATGTCTGG	GGCGCAGGGA	CCACGGTCAC	CGTCTCTGCA	2820
462							
463	GCTAGCACCA	AGGGCCCATC	GGTCTTCCCC	CTGGCACCCT	CCTCCAAGAG	CACCTCTGGG	2880
464							
465	GGCACAGCGG	CCCTGGGCTG	CCTGGTCAAG	GACTACTTCC	CCGAACCGGT	GACGGTGTCTG	2940
466							
467	TGGAACCTCAG	GCGCCCTGAC	CAGCGGCGTG	CACACCTTCC	CGGCTGTCCT	ACAGTCCTCA	3000
468							

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469	GGACTCTACT	CCCTCAGCAG	CGTGGTGACC	GTGCCCTCCA	GCAGCTTGGG	CACCCAGACC	3060
470							
471	TACATCTGCA	ACGTGAATCA	CAAGCCCAGC	AACACCAAGG	TGGACAAGAA	AGCAGAGCCC	3120
472							
473	AAATCTTGTG	ACAAAACTCA	CACATGCCCC	CCGTGCCCAG	CACCTGAACT	CCTGGGGGGA	3180
474							
475	CCGTCAGTCT	TCCTCTTCCC	CCCAAAAACCC	AAGGACACCC	TCATGATCTC	CCGGACCCCT	3240
476							
477	GAGGTCACAT	GCGTGGTGGT	GGACGTGAGC	CACGAAGACC	CTGAGGTCAA	GTTCAACTGG	3300
478							
479	TACGTGGACG	GCGTGGAGGT	GCATAATGCC	AAGACAAAGC	CGCGGGAGGA	GCAGTACAAC	3360
480							
481	AGCACGTACC	GTGTGGTCAG	CGTCCTCACC	GTCCTGCACC	AGGACTGGCT	GAATGGCAAG	3420
482							
483	GAGTACAAGT	GCAAGGTCTC	CAACAAAGCC	CTCCCAGCCC	CCATCGAGAA	AACCATCTCC	3480
484							
485	AAAGCCAAAG	GGCAGCCCCG	AGAACCACAG	GTGTACACCC	TGCCCCCATC	CCGGGATGAG	3540
486							
487	CTGACCAAGA	ACCAGGTCAG	CCTGACCTGC	CTGGTCAAAG	GCTTCTATCC	CAGCGACATC	3600
488							
489	GCCGTGGAGT	GGGAGAGCAA	TGGGCAGCCG	GAGAACAAC	ACAAGACCAC	GCCTCCCGTG	3660
490							
491	CTGGACTCCG	ACGGCTCCTT	CTTCCTCTAC	AGCAAGCTCA	COGTGGACAA	GAGCAGGTGG	3720
492							
493	CAGCAGGGGA	ACGTCTTCTC	ATGCTCCGTG	ATGCATGAGG	CTCTGCACAA	CCACTACACG	3780
494							
495	CAGAAGAGCC	TCTCCCTGTC	TCCGGGTAAA	TGAGGATCCG	TTAACGGTTA	CCAACTACCT	3840
496							
497	AGACTGGATT	CGTGACAACA	TGCGGCCGTG	ATATCTACGT	ATGATCAGCC	TCGACTGTGC	3900
498							
499	CTTCTAGTTG	CCAGCCATCT	GTTGTTTGCC	CCTCCCCCGT	GCCTTCCTTG	ACCCTGGAAG	3960
500							
501	GTGCCACTCC	CACTGTCCCTT	TCCTAATAAA	ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	4020
502							
503	GGTGTCAATC	TATTCTGGGG	GGTGGGGTGG	GGCAGGACAG	CAAGGGGGAG	GATTGGGAAG	4080
504							
505	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	GCTCTATGGA	ACCAGCTGGG	GCTCGACAGC	4140
506							
507	GCTGGATCTC	CCGATCCCCA	GCTTTGCTTC	TCAATTCTT	ATTGTCATAA	TGAGAAAAAA	4200
508							
509	AGGAAAATTA	ATTTTAACAC	CAATTCAGTA	GTTGATTGAG	CAAATGCGTT	GCCAAAAGG	4260
510							
511	ATGCTTTAGA	GACAGTGTTT	TCTGCACAGA	TAAGGACAAA	CATTATTCAG	AGGGAGTACC	4320
512							
513	CAGAGCTGAG	ACTCCTAAGC	CAGTGAGTGG	CACAGCATTC	TAGGGAGAAA	TATGCTTGTC	4380
514							
515	ATCACCGAAG	CCTGATTCCG	TAGAGCCACA	CCTTGGTAAG	GGCCAATCTG	CTCACACAGG	4440
516							
517	ATAGAGAGGG	CAGGAGCCAG	GGCAGAGCAT	ATAAGGTGAG	GTAGGATCAG	TTGCTCCTCA	4500
518							
519	CATTTGCTTC	TGACATAGTT	GTGTTGGGAG	CTTGGATAGC	TTGGACAGCT	CAGGGCTGCG	4560
520							

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521	ATTTCGCGCC	AAACTTGACG	GCAATCCTAG	CGTGAAGGCT	GGTAGGATTT	TATCCCCGCT	4620
522							
523	GCCATCATGG	TTCGACCATT	GAAGTGCATC	GTCGCCGTGT	CCCAAAATAT	GGGGATTGGC	4680
524							
525	AAGAACGGAG	ACCTACCCTG	GCCTCCGCTC	AGGAACGAGT	TCAAGTACTT	CCAAAGAATG	4740
526							
527	ACCACAACCT	CTTCAGTGGA	AGGTAAACAG	AATCTGGTGA	TTATGGGTAG	GAAAACCTGG	4800
528							
529	TTCTCCATTC	CTGAGAAGAA	TCGACCTTTA	AAGGACAGAA	TTAATATAGT	TCTCAGTAGA	4860
530							
531	GAAGTCAAAG	AACCACCACG	AGGAGCTCAT	TTTCTTGCCA	AAAGTTTGGA	TGATGCCTTA	4920
532							
533	AGACTTATTG	AACAACCGGA	ATTGGCAAGT	AAAGTAGACA	TGGTTTGGAT	AGTCGGAGGC	4980
534							
535	AGTTCTGTTT	ACCAGGAAGC	CATGAATCAA	CCAGGCCACC	TTAGACTCTT	TGTGACAAGG	5040
536							
537	ATCATGCAGG	AATTTGAAAG	TGACACGTTT	TTCCCAGAAA	TTGATTTGGG	GAAATATAAA	5100
538							
539	CTTCTCCCAG	AATACCCAGG	CGTCCTCTCT	GAGGTCCAGG	AGGAAAAAGG	CATCAAGTAT	5160
540							
541	AAGTTTGAAG	TCTACGAGAA	GAAAGACTAA	CAGGAAGATG	CTTCAAGTT	CTCTGCTCCC	5220
542							
543	CTCCTAAAGC	TATGCATTTT	TATAAGACCA	TGGGACTTTT	GCTGGCTTTA	GATCAGCCTC	5280
544							
545	GACTGTGCCT	TCTAGTTGCC	AGCCATCTGT	TGTTTGCCCC	TCCCCCGTGC	CTTCCTTGAC	5340
546							
547	CCTGGAAGGT	GCCACTCCCA	CTGTCCTTTC	CTAATAAAAT	GAGGAAATTG	CATCGCATTG	5400
548							
549	TCTGAGTAGG	TGTCATTCTA	TTCTGGGGGG	TGGGGTGGGG	CAGGACAGCA	AGGGGGAGGA	5460
550							
551	TTGGGAAGAC	AATAGCAGGC	ATGCTGGGGA	TGCGGTGGGC	TCTATGGAAC	CAGCTGGGGC	5520
552							
553	TCGAGCTACT	AGCTTTGCTT	CTCAATTTCT	TATTTGCATA	ATGAGAAAAA	AAGGAAAATT	5580
554							
555	AATTTTAACA	CCAATTCAGT	AGTTGATTGA	GCAAATGCGT	TGCCAAAAAG	GATGCTTTAG	5640
556							
557	AGACAGTGTT	CTCTGCACAG	ATAAGGACAA	ACATTATTCA	GAGGGAGTAC	CCAGAGCTGA	5700
558							
559	GACTCCTAAG	CCAGTGAGTG	GCACAGCATT	CTAGGGAGAA	ATATGCTTGT	CATCACCGAA	5760
560							
561	GCCTGATTCC	GTAGAGCCAC	ACCTTGGTAA	GGGCCAATCT	GCTCACACAG	GATAGAGAGG	5820
562							
563	GCAGGAGCCA	GGGCAGAGCA	TATAAGGTGA	GGTAGGATCA	GTTGCTCCTC	ACATTTGCTT	5880
564							
565	CTGACATAGT	TGTGTTGGGA	GCTTGGATCG	ATCCTCTATG	GTTGAACAAG	ATGGATTGCA	5940
566							
567	CGCAGGTTCT	CCGGCCGCTT	GGGTGGAGAG	GCTATTCGGC	TATGACTGGG	CACAACAGAC	6000
568							
569	AATCGGCTGC	TCTGATGCCG	CCGTGTTCCG	GCTGTCAGCG	CAGGGGCGCC	CGGTTCTTTT	6060
570							
571	TGTCAAGACC	GACCTGTCCG	GTGCCCTGAA	TGAACTGCAG	GACGAGGCAG	CGCGGCTATC	6120
572							

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573	GTGGCTGGCC	ACGACGGGCG	TTCCTTGCGC	AGCTGTGCTC	GACGTTGTCA	CTGAAGCGGG	6180
574							
575	AAGGGACTGG	CTGCTATTGG	GCGAAGTGCC	GGGGCAGGAT	CTCCTGTCAT	CTCACCTTGC	6240
576							
577	TCCTGCCGAG	AAAGTATCCA	TCATGGCTGA	TGCAATGCGG	CGGCTGCATA	CGCTTGATCC	6300
578							
579	GGCTACCTGC	CCATTGACC	ACCAAGCGAA	ACATCGCATC	GAGCGAGCAC	GTACTCGGAT	6360
580							
581	GGAAGCCGGT	CTTGTCGATC	AGGATGATCT	GGACGAAGAG	CATCAGGGGC	TCGCGCCAGC	6420
582							
583	CGAACTGTTC	GCCAGGCTCA	AGGCGCGCAT	GCCCCACGGC	GAGGATCTCG	TCGTGACCCA	6480
584							
585	TGGCGATGCC	TGCTTGCCGA	ATATCATGGT	GGAAAATGGC	CGCTTTTCTG	GATTCATCGA	6540
586							
587	CTGTGGCCGG	CTGGGTGTGG	CGGACCGCTA	TCAGGACATA	GCGTTGGCTA	CCCGTGATAT	6600
588							
589	TGCTGAAGAG	CTTGGCGGCG	AATGGGCTGA	CCGCTTCCTC	GTGCTTTACG	GTATCGCCGC	6660
590							
591	TCCCGATTTC	CAGCGCATCG	CCTTCTATCG	CCTTCTTGAC	GAGTTCTTCT	GAGCGGGACT	6720
592							
593	CTGGGGTTTC	AAATGACCGA	CCAAGCGACG	CCCAACCTGC	CATCACGAGA	TTTCGATTCC	6780
594							
595	ACCGCCGCCT	TCTATGAAAG	GTTGGGCTTC	GGAATCGTTT	TCCGGGACGC	CGGCTGGATG	6840
596							
597	ATCCTCCAGC	GCGGGGATCT	CATGCTGGAG	TTCTTCGCCC	ACCCCAACTT	GTTTATTGCA	6900
598							
599	GCTTATAATG	GTTACAAATA	AAGCAATAGC	ATCACAAATT	TCACAAATAA	AGCATTTTTTT	6960
600							
601	TCACTGCATT	CTAGTTGTGG	TTTGTCCAAA	CTCATCAATC	TATCTTATCA	TGTCTGGATC	7020
602							
603	GCGGCCGCGA	TCCCGTCGAG	AGCTTGCGCT	AATCATGGTC	ATAGCTGTTT	CCTGTGTGAA	7080
604							
605	ATTGTTATCC	GCTCACAATT	CCACACAACA	TACGAGCCGG	AAGCATAAAG	TGTAAAGCCT	7140
606							
607	GGGGTGCCCTA	ATGAGTGAGC	TAATCAGCAT	TAATTGCGTT	GCGCTCACTG	CCCCTTTTCC	7200
608							
609	AGTCGGGAAA	CCTGTCGTGC	CAGCTGCATT	AATGAATCGG	CCAACGCGCG	GGGAGAGGCG	7260
610							
611	GTTTGCGTAT	TGGGCGCTCT	TCCGCTTCCT	CGCTCACTGA	CTCGCTGCGC	TCGGTCGTTC	7320
612							
613	GGCTGCGGCG	AGCGGTATCA	GCTCACTCAA	AGGCGGTAAT	ACGGTTATCC	ACAGAATCAG	7380
614							
615	GGGATAACGC	AGGAAAGAAC	ATGTGAGCAA	AAGGCCAGCA	AAAGGCCAGG	AACCGTAAAA	7440
616							
617	AGGCCGCGTT	GCTGGCGTTT	TTCCATAGGC	TCCGCCCCC	TGACGAGCAT	CACAAAAATC	7500
618							
619	GACGCTCAAG	TCAGAGGTGG	CGAAACCCGA	CAGGACTATA	AAGATACCAG	GCGTTTCCCC	7560
620							
621	CTGGAAGCTC	CCTCGTGCGC	TCTCCTGTTC	CGACCCTGCC	GCTTACCGGA	TACCTGTCCG	7620
622							
623	CCTTTCTCCC	TTCGGGAAGC	GTGGCGCTTT	CTCAATGCTC	ACGCTGTAGG	TATCTCAGTT	7680
624							

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625	CGGTGTAGGT	CGTTCGCTCC	AAGCTGGGCT	GTGTGCACGA	ACCCCCCGTT	CAGCCCGACC	7740
626							
627	GCTGCGCCTT	ATCCGGTAAC	TATCGTCTTG	AGTCCAACCC	GGTAAGACAC	GACTTATCGC	7800
628							
629	CACTGGCAGC	AGCCACTGGT	AACAGGATTA	GCAGAGCGAG	GTATGTAGGC	GGTGCTACAG	7860
630							
631	AGTTCTTGAA	GTGGTGGCCT	AACTACGGCT	ACACTAGAAG	GACAGTATTT	GGTATCTGCG	7920
632							
633	CTCTGCTGAA	GCCAGTTACC	TTCGGAAAAA	GAGTTGGTAG	CTCTTGATCC	GGCAAACAAA	7980
634							
635	CCACCGCTGG	TAGCGGTGGT	TTTTTTGTTT	GCAAGCAGCA	GATTACGCGC	AGAAAAAAG	8040
636							
637	GATCTCAAGA	AGATCCTTTG	ATCTTTTCTA	CGGGGTCTGA	CGCTCAGTGG	AACGAAAAC	8100
638							
639	CACGTTAAGG	GATTTTGGTC	ATGAGATTAT	CAAAAAGGAT	CTTCACCTAG	ATCCTTTTAA	8160
640							
641	ATTAAAAATG	AAGTTTTTAA	TCAATCTAAA	GTATATATGA	GTAAACTTGG	TCTGACAGTT	8220
642							
643	ACCAATGCTT	AATCAGTGAG	GCACCTATCT	CAGCGATCTG	TCTATTTTCG	TCATCCATAG	8280
644							
645	TTGCCTGACT	CCCCGTCGTG	TAGATAACTA	CGATACGGGA	GGGCTTACCA	TCTGGCCCCA	8340
646							
647	GTGCTGCAAT	GATACCGCGA	GACCCACGCT	CACCGGCTCC	AGATTTATCA	GCAATAAACC	8400
648							
649	AGCCAGCCGG	AAGGGCCGAG	CGCAGAAGTG	GTCCTGCAAC	TTTATCCGCC	TCCATCCAGT	8460
650							
651	CTATTAATTG	TTGCCGGGAA	GCTAGAGTAA	GTAGTTCGCC	AGTTAATAGT	TTGCGCAACG	8520
652							
653	TTGTTGCCAT	TGCTACAGGC	ATCGTGGTGT	CACGCTCGTC	GTTTGGTATG	GCTTCATTCA	8580
654							
655	GCTCCGGTTC	CCAACGATCA	AGGCGAGTTA	CATGATCCCC	CATGTTGTGC	AAAAAAGCGG	8640
656							
657	TTAGCTCCTT	CGGTCTCCG	ATCGTTGTCA	GAAGTAAGTT	GGCCGCAGTG	TTTACTCTCA	8700
658							
659	TGGTTATGGC	AGCACTGCAT	AATTCTCTTA	CTGTCATGCC	ATCCGTAAGA	TGCTTTTCTG	8760
660							
661	TGACTGGTGA	GTACTCAACC	AAGTCATTCT	GAGAATAGTG	TATGCGGCGA	CCGAGTTGCT	8820
662							
663	CTTGCCCGGC	GTCAATACGG	GATAATACCG	CGCCACATAG	CAGAACTTTA	AAAGTGCTCA	8880
664							
665	TCATTGGAAG	ACGTTCTTCG	GGGCGAAAAA	TCTCAAGGAT	CTTACCGCTG	TTGAGATCCA	8940
666							
667	GTTTCGATGA	ACCCACTCGT	GCACCCAACT	GATCTTCAGC	ATCTTTTACT	TTCACCAGCG	9000
668							
669	TTTCTGGGTG	AGCAAAAACA	GGAAGGCAAA	ATGCCGCAAA	AAAGGGAATA	AGGGCGACAC	9060
670							
671	GGAAATGTTG	AATACTCATA	CTCTTCCTTT	TTCAATATTA	TTGAAGCATT	TATCAGGGTT	9120
672							
673	ATTGTCTCAT	GAGCGGATAC	ATATTTGAAT	GTATTTAGAA	AAATAAACAA	ATAGGGGTTC	9180
674							
675	CGCGCACATT	TCCCCGAAAA	GTGCCACCT				9209
676							

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677 (4)INFORMATION FOR SEQ. ID. NO.: 3:

678

679 (i)SEQUENCE CHARACTERISTICS:

680

681 (A)LENGTH: 54 bases

682 (B)TYPE: nucleic acid

683 (C)STRANDEDNESS: single

684 (D)TOPOLOGY: linear

685

686 (ii)MOLECULE TYPE: DNA (genomic)

687

688 (iii)HYPOTHETICAL: yes

689

690 (iv)ANTI-SENSE: no

691

692 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.: 3:

693

694 5' ATC ACA GAT CTC TCA CCA TGG ATT TTC AGG TBC AGA TTA TCA GCT52

695 TC 3' 2' *invalid* *This number needs to be 54.*

696

697

698 (5)INFORMATION FOR SEQ. ID. NO.: 4:

699

700 (i)SEQUENCE CHARACTERISTICS:

701

702 (A)LENGTH: 30 bases

703 (B)TYPE: nucleic acid

704 (C)STRANDEDNESS: single

705 (D)TOPOLOGY: linear

706

707 (ii)MOLECULE TYPE: DNA (genomic)

708

709 (iii)HYPOTHETICAL: yes

710

711 (iv)ANTI-SENSE: yes — *the above anti-sense is "no". Please verify these responses. PTO assumes that*

712

713 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.: 4:

714

715 *the sequence is 5' → 3'.*

716 5' TGC AGC ATC CGT ACG TTT GAT TTC CAG CTT 3' BO

717

718

719 (6)INFORMATION FOR SEQ. ID. NO.: 5:

720

721 (i)SEQUENCE CHARACTERISTICS:

722

723 (A)LENGTH: 384 bases

724 (B)TYPE: nucleic acid

725 (C)STRANDEDNESS: single

726 (D)TOPOLOGY: linear

727

728 (ii)MOLECULE TYPE: DNA (genomic)

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729
730 (iii)HYPOTHETICAL: yes
731
732 (iv)ANTI-SENSE: no
733
734 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.: 5:
735
736
737 ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA GTC 51
738
739 ATA ATG TCC AGA GGG CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC CTG TCT102
740
741 GCA TCT CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA153
742
743 AGT TAC ATC CAC TGG TTC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG204
744
745 ATT TAT GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT GTT CGC TTC AGT GGC255
746
747 AGT GGG TCT GGG ACT TCT TAC TCT CTC ACA ATC AGC AGA GTG GAG GCT GAR306
748
749 GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG ACT AGT AAC CCA CCC ACG TTC357
750
751 GGA GGG GGG ACC AAG CTG GAA ATC AAA384
752
753

754 (7)INFORMATION FOR SEQ. ID. NO.: 6:
755

756 (i)SEQUENCE CHARACTERISTICS:
757

758 (A)LENGTH: 27 bases
759 (B)TYPE: nucleic acid
760 (C)STRANDEDNESS: single
761 (D)TOPOLOGY: linear
762

763 (ii)MOLECULE TYPE: DNA (genomic)
764

765 (iii)HYPOTHETICAL: yes
766

767 (iv)ANTI-SENSE: no
768

769 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.: 6:
770

771
772 5' GCG GCT CCC ACG CGT GTC CTG TCC CAG 3'27
773
774
775
776

777 (8)INFORMATION FOR SEQ. ID. NO.: 7:
778

779 (i)SEQUENCE CHARACTERISTICS:
780

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781 (A)LENGTH: 29 bases
782 (B)TYPE: nucleic acid
783 (C)STRANDEDNESS: single
784 (D)TOPOLOGY: linear
785
786 (ii)MOLECULE TYPE: DNA (genomic)
787
788 (iii)HYPOTHETICAL: yes
789
790 (iv)ANTI-SENSE: yes
791
792 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.: 7:
793
794 5' GG(G/C) TGT TGT GCT AGC TG(A/C) (A/G)GA GAC (G/A)GT GA(3)29
795
796 use "N" and define the alternatives in the feature
797 (9)INFORMATION FOR SEQ. ID. NO.: 8:
798
799 (i)SEQUENCE CHARACTERISTICS:
800
801 (A)LENGTH: 420 bases
802 (B)TYPE: nucleic acid
803 (C)STRANDEDNESS: single
804 (D)TOPOLOGY: linear
805
806 (ii)MOLECULE TYPE: DNA (genomic)
807
808 (iii)HYPOTHETICAL: yes
809
810 (iv)ANTI-SENSE: no
811
812 (ix)SEQUENCE DESCRIPTION: SEQ. ID. NO.: 8:
813
814
815 ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT GTC 51
816
817 CTG TCC CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG CCT GGG102
818
819 GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT ACC AGT TAC153
820
821 AAT ATG CAC TGG GTA AAA CAG ACA CCT GGT CGG GGC CTG GAA TGG ATT GGA 204
822
823 GCT ATT TAT CCC GGA AAT GGT GAT ACT TCC TAC AAT CAG AAG TTC AAA GGC255
824
825 AAG GCC ACA TTG ACT GCA GAC AAA TCC TCC AGC ACA GCC TAC ATG CAG CTC306
826
827 AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAT TAC TGT GCA AGA TCG ACT357
828
829 TAC TAC GGC GGT GAC TGG TAC TTC AAT GTC TGG GGC GCA GGG ACC ACG GTC408
830 ACC GTC TCT GCA 420
831

All of these different
locations need to
be defined as an
N.

table
(ix) feature:

space